

## IN THE SPECIFICATION

Please **add** the following paragraph on page 1 line 5, following the title:

### CROSS REFERENCE TO RELATED APPLICATIONS

This application claims priority under 35 U.S.C. § 119(e) of U.S. Provisional Application No. 60/161,619, filed October 26, 1999.

Please **amend** the specification by replacing the paragraph on page 5, lines 16-25, with the following amended paragraph:

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ) (<http://www.ddbj.nig.ac.jp/>) ([www.ddbj.nig.ac.jp/](http://www.ddbj.nig.ac.jp/)); Genbank (<http://www.ncbi.nlm.nih.gov/web/Genbank/Index.html>) ([www.ncbi.nlm.nih.gov/web/Genbank/Index.html](http://www.ncbi.nlm.nih.gov/web/Genbank/Index.html)); and the European Molecular Biology Laboratory Nucleic Acid Sequence Database (EMBL) ([http://www.ebi.ac.uk/ebi\\_docs/embl\\_db.html](http://www.ebi.ac.uk/ebi_docs/embl_db.html)) ([www.ebi.ac.uk/ebi\\_docs/embl\\_db.html](http://www.ebi.ac.uk/ebi_docs/embl_db.html)). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designated for nucleotide sequences queries (BLASTN, BLASTX and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology*, 12: 76-80 (1994); Birren *et al.*, *Genome Analysis*, 1: 543-559 (1997)).